

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: FUNK, Walter D.
MacGILLIVRAY, Ross T.A.
MASON, Anne B.
WOODWORTH, Robert C.

(ii) TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
MOLECULES AND MUTANTS THEREOF

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street, suite 510
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 28-DEC-1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/832,029
(B) FILING DATE: 06-FEB-1992
(C) CLASSIFICATION: 1814

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: DeConti, Giulio A.
(B) REGISTRATION NUMBER: 31,503
(C) REFERENCE/DOCKET NUMBER: UVI-005CP2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 31..2124

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 88..2124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	TGTGCTCGCT GCTCAGCGCG CACCCGGAAG ATG AGG CTC GCC GTG GGA GCC CTG	54
	Met Arg Leu Ala Val Gly Ala Leu	
15	-19 -15	
	CTG GTC TGC GCC GTC CTG GGG CTG TGT CTG GCT GTC CCT GAT AAA ACT	102
	Leu Val Cys Ala Val Leu Gly Leu Cys Leu Ala Val Pro Asp Lys Thr	
	-10 -5 1 5	
20	GTG AGA TGG TGT GCA GTG TCG GAG CAT GAG GCC ACT AAG TGC CAG AGT	150
	Val Arg Trp Cys Ala Val Ser Glu His Glu Ala Thr Lys Cys Gln Ser	
	10 15 20	
25	TTC CGC GAC CAT ATG AAA AGC GTC ATT CCA TCC GAT GGT CCC AGT GTT	198
	Phe Arg Asp His Met Lys Ser Val Ile Pro Ser Asp Gly Pro Ser Val	
	25 30 35	
30	GCT TGT GTG AAG AAA GCC TCC TAC CTT GAT TGC ATC AGG GCC ATT GCG	246
	Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys Ile Arg Ala Ile Ala	
	40 45 50	
35	GCA AAC GAA GCG GAT GCT GTG ACA CTG GAT GCA GGT TTG GTC TAT GAT	294
	Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala Gly Leu Val Tyr Asp	
	55 60 65	
40	GCT TAC TTG GCT CCC AAT AAC CTG AAG CCT GTG GTG GCA GAG TTC TAT	342
	Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val Val Ala Glu Phe Tyr	
	70 75 80 85	
45	GGG TCA AAA GAG GAT CCA CAG ACT TTC TAT TAT GCT GTT GCT GTG GTG	390
	Gly Ser Lys Glu Asp Pro Gln Thr Phe Tyr Tyr Ala Val Ala Val Val	
	90 95 100	
50	AAG AAG GAT AGT GGC TTC CAG ATG AAC CAG CTT CGA GGC AAG AAG TCC	438
	Lys Lys Asp Ser Gly Phe Gln Met Asn Gln Leu Arg Gly Lys Lys Ser	
	105 110 115	
55	TGC CAC ACG GGT CTA GGC AGG TCC GCT GGG TGG AAC ATC CCC ATA GGC	486
	Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp Asn Ile Pro Ile Gly	
	120 125 130	
60	TTA CTT TAC TGT GAC TTA CCT GAG CCA CGT AAA CCT CTT GAG AAA GCA	534
	Leu Leu Tyr Cys Asp Leu Pro Glu Pro Arg Lys Pro Leu Glu Lys Ala	
	135 140 145	
65	GTG GCC AAT TTC TTC TCG GGC AGC TGT GCC CCT TGT GCG GAT GGG ACC	582
	Val Ala Asn Phe Phe Ser Gly Ser Cys Ala Pro Cys Ala Asp Gly Thr	
	150 155 160 165	

GenBank

	GAC	TTC	CCC	CAG	CTG	TGT	CAA	CTG	TGT	CCA	GGG	TGT	GGC	TGC	TCC	ACC	630
	Asp	Phe	Pro	Gln	Leu	Cys	Gln	Leu	Cys	Pro	Gly	Cys	Gly	Cys	Ser	Thr	
					170					175					180		
5	CTT	AAC	CAA	TAC	TTC	GGC	TAC	TCG	GGA	GCC	TTC	AAG	TGT	CTG	AAG	GAT	678
	Leu	Asn	Gln	Tyr	Phe	Gly	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Lys	Asp	
				185					190					195			
10	GGT	GCT	GGG	GAT	GTG	GCC	TTT	GTC	AAG	CAC	TCG	ACT	ATA	TTT	GAG	AAC	726
	Gly	Ala	Gly	Asp	Val	Ala	Phe	Val	Lys	His	Ser	Thr	Ile	Phe	Glu	Asn	
			200					205					210				
	TTG	GCA	AAC	AAG	GCT	GAC	AGG	GAC	CAG	TAT	GAG	CTG	CTT	TGC	CTA	GAC	774
15	Leu	Ala	Asn	Lys	Ala	Asp	Arg	Asp	Gln	Tyr	Glu	Leu	Leu	Cys	Leu	Asp	
		215					220					225					
	AAC	ACC	CGG	AAG	CCG	GTA	GAT	GAA	TAC	AAG	GAC	TGC	CAC	TTG	GCC	CAG	822
20	Asn	Thr	Arg	Lys	Pro	Val	Asp	Glu	Tyr	Lys	Asp	Cys	His	Leu	Ala	Gln	
	230					235					240					245	
	GTC	CCT	TCT	CAT	ACC	GTC	GTG	GCC	CGA	AGT	ATG	GGC	GGC	AAG	GAG	GAC	870
	Val	Pro	Ser	His	Thr	Val	Val	Ala	Arg	Ser	Met	Gly	Gly	Lys	Glu	Asp	
					250					255					260		
25	TTG	ATC	TGG	GAG	CTT	CTC	AAC	CAG	GCC	CAG	GAA	CAT	TTT	GGC	AAA	GAC	918
	Leu	Ile	Trp	Glu	Leu	Leu	Asn	Gln	Ala	Gln	Glu	His	Phe	Gly	Lys	Asp	
				265				270						275			
30	AAA	TCA	AAA	GAA	TTC	CAA	CTA	TTC	AGC	TCT	CCT	CAT	GGG	AAG	GAC	CTG	966
	Lys	Ser	Lys	Glu	Phe	Gln	Leu	Phe	Ser	Ser	Pro	His	Gly	Lys	Asp	Leu	
			280					285					290				
	CTG	TTT	AAG	GAC	TCT	GCC	CAC	GGG	TTT	TTA	AAA	GTC	CCC	CCA	AGG	ATG	1014
35	Leu	Phe	Lys	Asp	Ser	Ala	His	Gly	Phe	Leu	Lys	Val	Pro	Pro	Arg	Met	
		295					300					305					
	GAT	GCC	AAG	ATG	TAC	CTG	GGC	TAT	GAG	TAT	GTC	ACT	GCC	ATC	CGG	AAT	1062
40	Asp	Ala	Lys	Met	Tyr	Leu	Gly	Tyr	Glu	Tyr	Val	Thr	Ala	Ile	Arg	Asn	
	310					315					320					325	
	CTA	CGG	GAA	GGC	ACA	TGC	CCA	GAA	GCC	CCA	ACA	GAT	GAA	TGC	AAG	CCT	1110
	Leu	Arg	Glu	Gly	Thr	Cys	Pro	Glu	Ala	Pro	Thr	Asp	Glu	Cys	Lys	Pro	
					330					335					340		
45	GTG	AAG	TGG	TGT	GCG	CTG	AGC	CAC	CAC	GAG	AGG	CTC	AAG	TGT	GAT	GAG	1158
	Val	Lys	Trp	Cys	Ala	Leu	Ser	His	His	Glu	Arg	Leu	Lys	Cys	Asp	Glu	
				345				350						355			
50	TGG	AGT	GTT	AAC	AGT	GTA	GGG	AAA	ATA	GAG	TGT	GTA	TCA	GCA	GAG	ACC	1206
	Trp	Ser	Val	Asn	Ser	Val											

	AGC	TTG	GAT	GGA	GGG	TTT	GTC	TAC	ATA	GCG	GGC	AAG	TGT	GGT	CTG	GTG	1302
	Ser	Leu	Asp	Gly	Gly	Phe	Val	Tyr	Ile	Ala	Gly	Lys	Cys	Gly	Leu	Val	
	390					395					400					405	
5	CCT	GTC	TTG	GCA	GAA	AAC	TAC	AAT	AAG	AGC	GAT	AAT	TGT	GAG	GAT	ACA	1350
	Pro	Val	Leu	Ala	Glu	Asn	Tyr	Asn	Lys	Ser	Asp	Asn	Cys	Glu	Asp	Thr	
					410					415					420		
10	CCA	GAG	GCA	GGG	TAT	TTT	GCT	GTA	GCA	GTG	GTG	AAG	AAA	TCA	GCT	TCT	1398
	Pro	Glu	Ala	Gly	Tyr	Phe	Ala	Val	Ala	Val	Val	Lys	Lys	Ser	Ala	Ser	
				425					430					435			
15	GAC	CTC	ACC	TGG	GAC	AAT	CTG	AAA	GGC	AAG	AAG	TCC	TGC	CAT	ACG	GCA	1446
	Asp	Leu	Thr	Trp	Asp	Asn	Leu	Lys	Gly	Lys	Lys	Ser	Cys	His	Thr	Ala	
			440					445					450				
20	GTT	GGC	AGA	ACC	GCT	GGC	TGG	AAC	ATC	CCC	ATG	GGC	CTG	CTC	TAC	AAT	1494
	Val	Gly	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu	Tyr	Asn	
		455					460					465					
25	AAG	ATC	AAC	CAC	TGC	AGA	TTT	GAT	GAA	TTT	TTC	AGT	GAA	GGT	TGT	GCC	1542
	Lys	Ile	Asn	His	Cys	Arg	Phe	Asp	Glu	Phe	Phe	Ser	Glu	Gly	Cys	Ala	
	470					475					480					485	
30	CCT	GGG	TCT	AAG	AAA	GAC	TCC	AGT	CTC	TGT	AAG	CTG	TGT	ATG	GGC	TCA	1590
	Pro	Gly	Ser	Lys	Lys	Asp	Ser	Ser	Leu	Cys	Lys	Leu	Cys	Met	Gly	Ser	
					490					495				500			
35	GGC	CTA	AAC	CTG	TGT	GAA	CCC	AAC	AAC	AAA	GAG	GGA	TAC	TAC	GGC	TAC	1638
	Gly	Leu	Asn	Leu	Cys	Glu	Pro	Asn	Asn	Lys	Glu	Gly	Tyr	Tyr	Gly	Tyr	
				505					510					515			
40	ACA	GGC	GCT	TTC	AGG	TGT	CTG	GTT	GAG	AAG	GGA	GAT	GTG	GCC	TTT	GTG	1686
	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Val	Glu	Lys	Gly	Asp	Val	Ala	Phe	Val	
			520					525					530				
45	AAA	CAC	CAG	ACT	GTC	CCA	CAG	AAC	ACT	GGG	GGA	AAA	AAC	CCT	GAT	CCA	1734
	Lys	His	Gln	Thr	Val	Pro	Gln	Asn	Thr	Gly	Gly	Lys	Asn	Pro	Asp	Pro	
		535					540					545					
50	TGG	GCT	AAG	AAT	CTG	AAT	GAA	AAA	GAC	TAT	GAG	TTG	CTG	TGC	CTT	GAT	1782
	Trp	Ala	Lys	Asn	Leu	Asn	Glu	Lys	Asp	Tyr	Glu	Leu	Leu	Cys	Leu	Asp	
	550					555				560					565		
55	GGT	ACC	AGG	AAA	CCT	GTG	GAG	GAG	TAT	GCG	AAC	TGC	CAC	CTG	GCC	AGA	1830
	Gly	Thr	Arg	Lys	Pro	Val	Glu	Glu	Tyr	Ala	Asn	Cys	His	Leu	Ala	Arg	
					570					575				580			
60	GCC	CCG	AAT	CAC	GCT	GTG	GTC	ACA	CGG	AAA	GAT	AAG	GAA	GCT	TGC	GTC	1878
	Ala	Pro	Asn	His	Ala	Val	Val	Thr	Arg	Lys	Asp	Lys	Glu	Ala	Cys	Val	
				585					590					595			
65	CAC	AAG	ATA	TTA	CGT	CAA	CAG	CAG	CAC	CTA	TTT	GGA	AGC	AAC	GTA	ACT	1926
	His	Lys	Ile	Leu	Arg	Gln	Gln	Gln	His	Leu	Phe	Gly	Ser	Asn	Val	Thr	
			600					605					610				
70	GAC	TGC	TCG	GGC	AAC	TTT	TGT	TTG	TTC	CGG	TCG	GAA	ACC	AAG	GAC	CTT	1974
	Asp	Cys	Ser	Gly	Asn	Phe	Cys	Leu	Phe	Arg	Ser	Glu	Thr	Lys	Asp	Leu	
		615					620					625					

	CTG	TTC	AGA	GAT	GAC	ACA	GTA	TGT	TTG	GCC	AAA	CTT	CAT	GAC	AGA	AAC	2022
	Leu	Phe	Arg	Asp	Asp	Thr	Val	Cys	Leu	Ala	Lys	Leu	His	Asp	Arg	Asn	
	630					635				640						645	
5	ACA	TAT	GAA	AAA	TAC	TTA	GGA	GAA	GAA	TAT	GTC	AAG	GCT	GTT	GGT	AAC	2070
	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Glu	Glu	Tyr	Val	Lys	Ala	Val	Gly	Asn	
					650					655						660	
10	CTG	AGA	AAA	TGC	TCC	ACC	TCA	TCA	CTC	CTG	GAA	GCC	TGC	ACT	TTC	CGT	2118
	Leu	Arg	Lys	Cys	Ser	Thr	Ser	Ser	Leu	Leu	Glu	Ala	Cys	Thr	Phe	Arg	
					665					670						675	
	AGA	CCT	TAA	AATCTCA	GAGGTAGGGC	TGCCACCAAG	GTGAAGATGG	GAACGCAGAT									2174
15	Arg	Pro															
	GATCCATGAG	TTTGCCCTGG	TTTCACTGGC	CCAAGTGGTT	TGTGCTAACC	ACGTCTGTCT											2234
20	TCACAGCTCT	GTGTTGCCAT	GTGTGCTGAA	CAAAAAATAA	AAATTATTAT	TGATTTTATA											2294
	TTTCAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA													2327
25	(2)	INFORMATION	FOR	SEQ	ID	NO:2:											
	(i)	SEQUENCE	CHARACTERISTICS:														
		(A)	LENGTH:	698	amino	acids											
		(B)	TYPE:	amino	acid												
30		(D)	TOPOLOGY:	linear													
	(ii)	MOLECULE	TYPE:	protein													
	(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:2:											
35	Met	Arg	Leu	Ala	Val	Gly	Ala	Leu	Leu	Val	Cys	Ala	Val	Leu	Gly	Leu	
	-19				-15					-10					-5		
	Cys	Leu	Ala	Val	Pro	Asp	Lys	Thr	Val	Arg	Trp	Cys	Ala	Val	Ser	Glu	
40				1				5					10				
	His	Glu	Ala	Thr	Lys	Cys	Gln	Ser	Phe	Arg	Asp	His	Met	Lys	Ser	Val	
		15					20					25					
45	Ile	Pro	Ser	Asp	Gly	Pro	Ser	Val	Ala	Cys	Val	Lys	Lys	Ala	Ser	Tyr	
	30					35					40					45	
	Leu	Asp	Cys	Ile	Arg	Ala	Ile	Ala	Ala	Asn	Glu	Ala	Asp	Ala	Val	Thr	
					50					55						60	
50	Leu	Asp	Ala	Gly	Leu	Val	Tyr	Asp	Ala	Tyr	Leu	Ala	Pro	Asn	Asn	Leu	
				65					70						75		
	Lys	Pro	Val	Val	Ala	Glu	Phe	Tyr	Gly	Ser	Lys	Glu	Asp	Pro	Gln	Thr	
55			80					85					90				
	Phe	Tyr	Tyr	Ala	Val	Ala	Val	Val	Lys	Lys	Asp	Ser	Gly	Phe	Gln	Met	
		95					100					105					

Ala Val Val Lys Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys
430 435 440 445

5 Gly Lys Lys Ser Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn
450 455 460

Ile Pro Met Gly Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp
465 470 475

10 Glu Phe Phe Ser Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser
480 485 490

15 Leu Cys Lys Leu Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn
495 500 505

Asn Lys Glu Gly Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val
510 515 520 525

20 Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn
530 535 540

Thr Gly Gly Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys
545 550 555

25 Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu
560 565 570

30 Tyr Ala Asn Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr
575 580 585

Arg Lys Asp Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln
590 595 600 605

35 His Leu Phe Gly Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu
610 615 620

Phe Arg Ser Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys
625 630 635

40 Leu Ala Lys Leu His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu
640 645 650

45 Glu Tyr Val Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser
655 660 665

Leu Leu Glu Ala Cys Thr Phe Arg Arg Pro
670 675

50 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 GCAGAAACT ACGATAAGAG CGATAAT

27

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

20 CTATTTGGAA GCGACGTAAC TGACTGC

27

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser
1 5 10

40

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55 Val Pro Asp Lys Thr Val Arg Trp Xaa Ala Val Ser
1 5 10

5

10

15

Val Pro Asp Lys Thr Val
1 5